



CDS: isp6



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General Information

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Name isp6
Systematic Name SPAC4A8.04
Gene Synonyms prb1
Status experimentally characterised (or published)
Product vacuolar serine protease Isp6
Type CDS
Sequence [DNA](#) and [Protein](#)

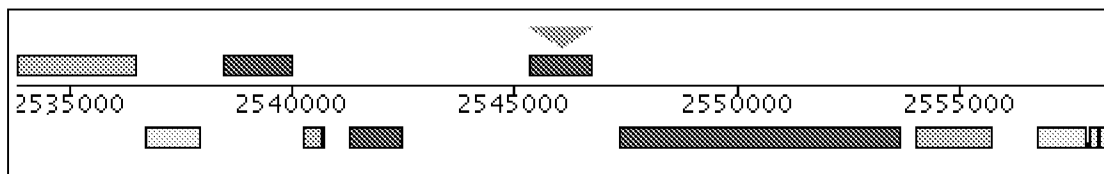
Location

Chromosome 1
Contig Location 2545350..2546753 (Unspliced length: 1404 bp)
Exons 2545350..2546753 (Spliced length: 1404 bp)

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Context Map:



SPAC25H1.07 SPAC25H1.08c mde5 SPAC4A8.02c ptc4 >isp6< myp2 SPAC4A8.06c SPAC4A8.07c

Curation

Term
 expressed during nitrogen starvation
 conserved eukaryotic family
 similar to *S. cerevisiae* YEL060C
 similar to *S. pombe* SPAC1006.01

Db xref/URL
[PMID:11872168](#)

Other genes annotated to this term
 (2 Others)
 (866 Others)
 (1 Other)
 (0 Others)

Predicted Peptide Properties

Mass	49.3 kDa	Amino acids	467
Isoelectric point	pH 5.2	Charge	-12.0

Signal Peptide Signal peptide predicted for SPAC4A8.04 by SignalP 2.0 HMM (Signal peptide probability 0.999, signal anchor probability 0.000) with cleavage site probability 0.874 between residues 24 and 25

Transmembrane Domains	0 found
GPI Anchor	GPI-Anchor Signal predicted for SPAC4A8.04 by DGPI v2.04 with cleavage site probability 1.5480001 near 430

Gene Ontology Annotation

Term (browse Amigo)	Qualifier Evidence	Other genes annotated to this term
Biological Process		
RNA catabolic process	IGI (PMID:11872168) with pnu1	75 others
autophagy	IMP (PMID:16550352)	24 others
cellular response to nitrogen starvation	IEP (PMID:11872168)	30 others
cellular response to nitrogen starvation	IMP (PMID:16550352)	30 others
conjugation with cellular fusion	IMP (PMID:7954893)	103 others
proteolysis involved in cellular protein catabolic process	IMP (PMID:11872168)	167 others
regulation of nitrogen compound metabolic process	IMP (PMID:16550352)	5 others
vacuole organization and biogenesis	IMP (PMID:16550352)	44 others
Cellular Component		
Golgi apparatus	IDA (PMID:16823372)	356 others
vacuole	TAS (PMID:16550352)	145 others
Molecular Function		
serine-type endopeptidase activity	IEA (GOA:spkw GO_REF:00000004) with SP_KW:KW-0720	13 others
serine-type peptidase activity	ISS (PMID:17072883) with Pfam:PF00082	18 others

Catalytic Activity
EC 3.4.21.- : [IUBMB](#)EC 3.4.24.- : [IUBMB](#)

Published Expression Profiles

Gene Expression Viewer [Cell Cycle](#) [Meiosis](#) [Environmental Stress](#) [Pheromone Response/Mating](#)
TranscriptomeViewer [SPAC4A8.04](#) High-resolution view of transcripts in neighbourhood

Literature
Search for [isp6](#) in PubMed

Domain Information
[View Pfam domain structure for this gene product](#)[View SCOP superfamily](#)

DB	Accs	Description
Pfam	PF05922	Subtilisin N-terminal Region
Pfam	PF00082	Subtilase family
MEROPS	S08.052	MEROPS
InterPro	IPR000209	Peptidase S8 and S53, subtilisin, kexin, sedolisin
InterPro	IPR010259	Proteinase inhibitor I9, subtilisin propeptide
InterPro	IPR015500	Subtilisin-related serine protease

PRINTS	PR00723	Subtilisin serine protease family (S8) signature
PROSITE	PS00136	Serine proteases, subtilase family, aspartic acid active site.
PROSITE	PS00137	Serine proteases, subtilase family, histidine active site.
PROSITE	PS00138	Serine proteases, subtilase family, serine active site.

Database Cross-References

DB	Accs	Description
UniProtKB	P40903	Sexual differentiation process putative subtilase-type proteinase isp6 (EC 3.4.21.-).
EMBL	D14063	Schizosaccharomyces pombe mRNA for serine protease, complete cds.
EMBL	CU329670	Schizosaccharomyces pombe chromosome I
Biotwiki	SPAC4A8.04	Biotwiki
NCBI Entrez Gene	SPAC4A8.04	NCBI Entrez Gene
FYSSION	SPAC4A8.04	FYSSION
GermOnline	SPAC4A8.04	GermOnline
NBRP	SPAC4A8.04	Fission yeast strain database, National BioResource Project (Japan)
PIR	S45493	PIR
YOGY	SPAC4A8.04	Retrieval of eukaryotic orthologs

UniProtKB Annotation For This Protein

Developmental Stage	Transcribed specifically during sexual development.
Similarity	Belongs to the peptidase S8 family.
Keywords	Complete proteome (4982 others) , Hydrolase (451 others) , Protease (90 others) , Serine protease (8 others)

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